

SEQUENCE LISTING



#4
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TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Wahl, Geoffrey M
O'Gorman, Stephen V

(ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
THEREFOR

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
(B) STREET: 444 South Flower Street, Suite 2000
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/484,324
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E
(B) REGISTRATION NUMBER: 31,192
(C) REFERENCE/DOCKET NUMBER: P41 9984

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 546-4737
(B) TELEFAX: (619) 546-9392

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NATIVE FLP

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT	48
Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val	
1 5 10 15	
CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA	96
Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala	
20 25 30	
TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC	144
Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn	
35 40 45	
GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA	192
Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile	
50 55 60	
AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA	240
Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys	
65 70 75 80	
TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG	288
Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu	
85 90 95	
ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT	336
Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His	
100 105 110	
CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA	384
Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu	
115 120 125	
TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT	432
Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu	
130 135 140	
AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA	480
Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys	
145 150 155 160	
ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT	528
Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr	
165 170 175	
TTA TAC CAA TTC CTC TTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC	576
Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe	
180 185 190	
AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TTT AAA TTA GTC CAA AAT	624
Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn	

195	200	205	
AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr 210 215 220			672
AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp 225 230 235 240			720
CCA CTT GTA TAT TTG GAT GAA TTT TTG AGG AAT TCT GAA CCA GTC CTA Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu 245 250 255			768
AAA CGA GTA AAT AGG ACC GGC AAT TCT TCA AGC AAT AAA CAG GAA TAC Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr 260 265 270			816
CAA TTA TTA AAA GAT AAC TTA GTC AGA TCG TAC AAT AAA GCT TTG AAG Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys 275 280 285			864
AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCT Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser 290 295 300			912
CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu 305 310 315 320			960
ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser 325 330 335			1008
GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAT Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp 340 345 350			1056
CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TCA His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser 355 360 365			1104
AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TGG Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp 370 375 380			1152
CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr 385 390 395 400			1200
CCC GCA TGG ATT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser 405 410 415			1248
TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT Ser Tyr Ile Asn Arg Arg Ile 420			1299

ATCCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA 1359
ACAGTGAGCT GTATGTGCGC A 1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu	Val	1	5	10	15
Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys	Ile	Ala	20	25	30	
Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile	Thr	His	Asn	35	40	45	
Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr	Asn	Thr	Ile	Ile	50	55	60	
Ser	Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn	Lys	Ser	Leu	Gln	Phe	Lys	65	70	75	80
Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu	Ala	Ser	Leu	Lys	Lys	Leu	85	90	95	
Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile	Pro	Tyr	Tyr	Gly	Gln	Lys	His	100	105	110	
Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val	Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	115	120	125	
Ser	Ser	Glu	Glu	Ala	Asp	Lys	Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	130	135	140	
Lys	Ala	Leu	Leu	Ser	Glu	Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	145	150	155	160
Ile	Leu	Asn	Ser	Phe	Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	165	170	175	
Leu	Tyr	Gln	Phe	Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	180	185	190	
Ser	Asp	Ile	Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	195	200	205	
Lys	Tyr	Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr				

210	215	220
Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp		
225	230	235 240
Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu		
	245	250 255
Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr		
	260	265 270
Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys		
	275	280 285
Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser		
	290	295 300
His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu		
305	310	315 320
Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser		
	325	330 335
Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp		
	340	345 350
His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser		
	355	360 365
Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp		
	370	375 380
Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr		
385	390	395 400
Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser		
	405	410 415
Ser Tyr Ile Asn Arg Arg Ile		
	420	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG	60
GAACTTCA	68